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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/889,738

DATE: 12/11/2001

TIME: 14:56:21

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF3\12112001\I889738.raw

ENTERED

3 <110> APPLICANT: Gressel, Jonathan
4 Eyal, Yoram
5 Fluhr, Robert
7 <120> TITLE OF INVENTION: RHAMNOSYL-TRANSFERASE GENE AND USES THEREOF
9 <130> FILE REFERENCE: 01/22289
11 <140> CURRENT APPLICATION NUMBER: US 09/889,738
12 <141> CURRENT FILING DATE: 2000-01-20
14 <150> PRIOR APPLICATION NUMBER: IL 128193
15 <151> PRIOR FILING DATE: 1999-01-20
17 <150> PRIOR APPLICATION NUMBER: PCT/IL00/00038
18 <151> PRIOR FILING DATE: 2000-01-20
20 <160> NUMBER OF SEQ ID NOS: 21
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 8
26 <212> TYPE: PRT
27 <213> ORGANISM: Citrus X paradisi
29 <400> SEQUENCE: 1
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32 1 5
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38 <213> ORGANISM: Citrus X paradisi
40 <400> SEQUENCE: 2
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43 1
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48 <212> TYPE: PRT
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51 <400> SEQUENCE: 3
53 Ile Ala Ala Ile Leu Phe Leu
54 1 5
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58 <211> LENGTH: 8
59 <212> TYPE: PRT
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70 <212> TYPE: PRT
71 <213> ORGANISM: Citrus X paradisi
73 <400> SEQUENCE: 5
75 Glu Lys Met Thr Ile Glu Glu Ala

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79 <210> SEQ ID NO: 6
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81 <212> TYPE: PRT
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84 <400> SEQUENCE: 6
86 Leu Phe Gln Pro
87 1
90 <210> SEQ ID NO: 7
91 <211> LENGTH: 14
92 <212> TYPE: PRT
93 <213> ORGANISM: Citrus X paradisi
95 <400> SEQUENCE: 7
97 Val Val Asp Asn Gly Met Gly Met Val Val Pro Arg Asp Lys
98 1          5          10
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103 <212> TYPE: DNA
104 <213> ORGANISM: Artificial sequence
106 <220> FEATURE:
107 <223> OTHER INFORMATION: Synthetic oligonucleotide
109 <220> FEATURE:
110 <221> NAME/KEY: misc_feature
111 <222> LOCATION: (9)..(9)
112 <223> OTHER INFORMATION: Modified base : Inosine
115 <220> FEATURE:
116 <221> NAME/KEY: misc_feature
117 <222> LOCATION: (15)..(15)
118 <223> OTHER INFORMATION: Modified base : Inosine
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W--> 122 gayaayggna tgggnatggt                20
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126 <211> LENGTH: 7
127 <212> TYPE: PRT
128 <213> ORGANISM: Citrus X paradisi
130 <400> SEQUENCE: 9
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133 1          5
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137 <211> LENGTH: 23
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Synthetic oligonucleotide
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146 <222> LOCATION: (12)..(12)
147 <223> OTHER INFORMATION: Modified base: Inosine
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W--> 151 garaaratga cnathgarga rgc 23
154 <210> SEQ ID NO: 11
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156 <212> TYPE: DNA
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159 <220> FEATURE:
160 <223> OTHER INFORMATION: Synthetic oligonucleotide
162 <220> FEATURE:
163 <221> NAME/KEY: misc_feature
164 <222> LOCATION: (12)..(12)
165 <223> OTHER INFORMATION: Modified base : Inosine
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169 <221> NAME/KEY: misc_feature
170 <222> LOCATION: (18)..(18)
171 <223> OTHER INFORMATION: Modified base : Inosine
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175 <221> NAME/KEY: misc_feature
176 <222> LOCATION: (21)..(21)
177 <223> OTHER INFORMATION: Modified base : Inosine
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189 <400> SEQUENCE: 12
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192 1 5
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196 <211> LENGTH: 33
197 <212> TYPE: DNA
198 <213> ORGANISM: Artificial sequence
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201 <223> OTHER INFORMATION: Synthetic oligonucleotide
203 <400> SEQUENCE: 13
204 gttttccag tcacgacgtt tttttttttt ttt 33
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208 <211> LENGTH: 18
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210 <213> ORGANISM: Artificial sequence
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213 <223> OTHER INFORMATION: Synthetic oligonucleotide
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219 <210> SEQ ID NO: 15
220 <211> LENGTH: 18
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial sequence
224 <220> FEATURE:

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231 <210> SEQ ID NO: 16
232 <211> LENGTH: 18
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: Synthetic oligonucleotide
239 <400> SEQUENCE: 16
240 gacaatggta tgggcatg 18
243 <210> SEQ ID NO: 17
244 <211> LENGTH: 24
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Synthetic oligonucleotide
251 <400> SEQUENCE: 17
252 cctcaaccac cgagcccaa ccac 24
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257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial sequence
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268 <211> LENGTH: 29
269 <212> TYPE: DNA
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273 <223> OTHER INFORMATION: Synthetic oligonucleotide
275 <400> SEQUENCE: 19
276 caggatcctt attcagattt cttgacaag 29
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280 <211> LENGTH: 1359
281 <212> TYPE: DNA
282 <213> ORGANISM: Citrus X paradisi
284 <400> SEQUENCE: 20
285 atggatacca agcatcaaga taagccaagc attctcatgt taccatggct agctcatggg 60
287 cacatagctc cacaccttga acttgccaag aagctttcac agaaaaactt ccacatatat 120
289 ttctgctcta ctccaacaa tctacaatcc ttcggcagaa atgttgaaaa aaacttctca 180
291 tcttcaatac aactcataga actgcaactt cccaatacat tccctgaact tccttcacaa 240
293 aatcagacca caaaaaacct tcctcccat cttatttata ctctcgtggg agcatttgaa 300
295 gacgcaaaac ctgctttttg caacatcttg gagacgetta aaccaaccct tgttatgtat 360
297 gatttggttc aaccgatggc ggcggaggca gcttaccagt atgacatagc tgctattttg 420
299 ttcttaccct tatctgcagt agcctgctct ttcttgctgc acaatatcgt aaatcccagc 480
301 ctgaaatacc ctttctttga atctgattac caagatagag aaagcaagaa catcaattac 540

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303 ttctgcac ttactgccaa tggcacctta aacaaagaca ggttcttaaa agctttcgaa 600
305 ctatcttgca aatttggtgt catcaaaaca tcaagagaga ttgaatccaa gtacttggat 660
307 tattttcctt ctttaatggg aaatgaaata attccagtag ggctctaat ccaagaacct 720
309 accttcaagg tagatgatac aaagatcatg gactggctga gccaaaagga gcctcgttca 780
311 gtcgtgtatg catccttttg cagtgaagtac ttctcttcca cggatgaaat acatgacata 840
313 gctattgggt tattgtcac cgaggttaat tttatatggg ctttcagatt acatcctgat 900
315 gagaaaatga cgatagagga agcactgcct cagggctttg ctgaggagat tgaaaggaat 960
317 aataagggaa tgatagtaca aggttgggtt ccgcaggcta aaattttaag gcatggaagc 1020
319 atcggcggat ttttgagtca ttgtggttg ggctcggtg ttgaggggat ggttttcggg 1080
321 gtaccaatca taggtgtgcc aatggcatat gagcagccaa gcaatgccaa ggtggtggtt 1140
323 gacaatggta tgggcatggt cgttccaaga gataagatca atcaaagact tggaggagag 1200
325 gaggtggcga gggtcattaa acatgtttgt ctgcaagaag aagcgaagca aataagaaga 1260
327 aaagctaata aaattagtga gagtatgaag aagatagggg acgcacagat gagtgtggtg 1320
329 gtggagaaac tgctgcagct tgtcaagaaa tctgaataa 1359
332 <210> SEQ ID NO: 21
333 <211> LENGTH: 452
334 <212> TYPE: PRT
335 <213> ORGANISM: Citrus X paradisi
337 <400> SEQUENCE: 21
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340 1 5 10 15
343 Leu Ala His Gly His Ile Ala Pro His Leu Glu Leu Ala Lys Lys Leu
344 20 25 30
347 Ser Gln Lys Asn Phe His Ile Tyr Phe Cys Ser Thr Pro Asn Asn Leu
348 35 40 45
351 Gln Ser Phe Gly Arg Asn Val Glu Lys Asn Phe Ser Ser Ser Ile Gln
352 50 55 60
355 Leu Ile Glu Leu Gln Leu Pro Asn Thr Phe Pro Glu Leu Pro Ser Gln
356 65 70 75 80
359 Asn Gln Thr Thr Lys Asn Leu Pro Pro His Leu Ile Tyr Thr Leu Val
360 85 90 95
363 Gly Ala Phe Glu Asp Ala Lys Pro Ala Phe Cys Asn Ile Leu Glu Thr
364 100 105 110
367 Leu Lys Pro Thr Leu Val Met Tyr Asp Leu Phe Gln Pro Met Ala Ala
368 115 120 125
371 Glu Ala Ala Tyr Gln Tyr Asp Ile Ala Ala Ile Leu Phe Leu Pro Leu
372 130 135 140
375 Ser Ala Val Ala Cys Ser Phe Leu Leu His Asn Ile Val Asn Pro Ser
376 145 150 155 160
379 Leu Lys Tyr Pro Phe Phe Glu Ser Asp Tyr Gln Asp Arg Glu Ser Lys
380 165 170 175
383 Asn Ile Asn Tyr Phe Leu His Leu Thr Ala Asn Gly Thr Leu Asn Lys
384 180 185 190
387 Asp Arg Phe Leu Lys Ala Phe Glu Leu Ser Cys Lys Phe Val Phe Ile
388 195 200 205
391 Lys Thr Ser Arg Glu Ile Glu Ser Lys Tyr Leu Asp Tyr Phe Pro Ser
392 210 215 220
395 Leu Met Gly Asn Glu Ile Pro Val Gly Pro Leu Ile Gln Glu Pro
396 225 230 235 240

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VERIFICATION SUMMARY

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L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11